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SHORT NOTES

Evidence of linkage between two egg albumen loci in the domestic fowl

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Genetic polymorphism in the egg white proteins of the domestic fowl was shown to exist by Lush (1961), using starch gel electrophoresis. He observed several phenotypes and suggested that these were controlled by three autosomal loci with two alleles at each locus.

In the work reported here, a strain of White Leghorns of the School of Agriculture, Edinburgh, was surveyed for egg albumen types by starch gel electrophoresis. This strain was built up from ten males and ten females in 1955 and a similar number in 1956. It has been closed since then, and the flock built up to a thousand in 1957. Since 1957, the flock has been random bred and the population surveyed was the fifth random bred generation of this strain.

Electrophoresis was carried out using the buffer system of Poulik (1957), slightly modified (Lush, 1961). The gels, 22·75 cm. × 19·75 cm. × 0·3 cm., each accommodated twenty albumen samples. A stabilized voltage gradient of 10 to 12 V/cm. was established across the gel for 4 to 5 hours at a room temperature of 4° C.

Genetic variation was observed in two of the loci described by Lush (1961); the ovalbumin locus (locus *I*) and locus *II*. The classification of ovalbumin phenotypes is described by Lush (1964). There was no genetic variation in locus *III* or in the transferrin locus of Ogden *et al.* (1962), all birds being of type IIIB, Tf-b. The birds were classified on their phenotypes, and the data are given in Table 1. The gene frequencies for the alleles at the two loci, shown in Table 2, indicate that the population is in Hardy-Weinberg equilibrium for each locus considered separately. The expectations calculated on the basis of independent segregation differ significantly from the observed values (linkage $\chi^2 = 154{\cdot}9$, $P < 0{\cdot}001$).

Table 1. *Classification of hens with reference to the ovalbumin locus and locus* II.

		OVALBUMIN LOCUS			
		AA	AB	BB	TOTAL
LOCUS *II*	AA	160	333	196	689
	AB	108	130	0	238
	BB	22	0	0	22
	TOTAL	290	463	196	949

	χ^2	D.F.
Segregation for Ov. locus	0·202	1
Segregation for locus *II*	0·072	1
Linkage	154·9	4

Table 2. *Gene frequencies at the ovalbumin locus and locus* II

	A	B
Ovalbumin locus	0·55	0·45
Locus *II*	0·85	0·15

The data in Table 1 indicate that all Ov B homozygotes are also II A homozygotes. This would be explained by an absence of the gametic type $Ov^B II^B$ in this population. If this gametic type is absent, the frequencies of the other three possible gametic types can be worked out by the maximum likelihood method. The frequencies estimated by this method are shown in Table 3.

From a knowledge of these gametic frequencies the expected number of individuals in each class can be calculated. The results given in Table 4 indicate that the expectation is a good fit to observed data ($\chi^2 = 0{\cdot}73$, $P > 0{\cdot}95$).

Table 3. *Maximum likelihood estimates of gametic frequencies (assuming gametic type* $Ov^B II^B$ *to be absent)*

$Ov^A II^A$	0·397
$Ov^A II^B$	0·150
$Ov^B II^A$	0·453

Table 4. *Comparison of actual and expected numbers in each class assuming gametic frequencies of Table* 3

		AA		AB		BB	
		Act.	Exp.	Act.	Exp.	Act.	Exp.
Locus *II*	AA	160	149·4	333	341·3	196	196·0
	AB	108	113·0	130	129·1	0	0
	BB	22	21·4	0	0	0	0

	χ^2	D.F.
Segregation for Ov. locus	0·157	1
Segregation for locus II	0·106	1
Correlation	0·727	4

It is unlikely that the absence of some classes is due to some gene combinations being lethal, as Lush (1961) found birds in two of these classes in the BR (Breeding) line of Brown Leghorns kept at this laboratory.

As the population was built up from a very small initial sample of birds, it is possible that, though the combination $Ov^B II^B$ was present in the population from which the sample came, it was by chance absent from the sample. If this were so and the two loci were linked, then some gametes of this type should have been formed by crossing-over in heterozygotes of the type $Ov^A II^B / Ov^B II^A$ and the frequency of this gamete in the flock would have gradually increased. It can be estimated that about 600 birds, which were the progeny of such heterozygotes, must occur in the ancestry of the present generation. Since no $Ov^B II^B$ gametes were detected in the present sample, the distance between the two loci must be less than one cross-over unit.

In the absence of evidence of crossing over, the observed results could be explained on the basis of a single locus with multiple alleles, three of which are present in this White Leghorn flock, with each allele controlling two regions in the electrophoretic pattern;

region I and region II of Lush (1961). On this postulate, one gene would produce several protein fractions differing in electrophoretic mobilities. If this gene mutates, one would expect all the fractions to change as they would now have different mobilities from the original gene products. Since there are strains existing in which either region I or region II is fixed and variation occurs only in one region, the theory of a multiple allelic locus seems very improbable.

SUMMARY

The ovalbumin locus and locus *II* (Lush, 1961) were found to segregate in a closed flock of White Leghorns. Three of the nine expected genotypic classes were absent and from this it is concluded that the two loci are very tightly linked.

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